

# FIG. 1A

```

ctatagggaa agctggtacg cctgcaggta ccggtccgga aattcgcggc cgcgtcgacg -53
ggtagagtcg ctgagggccc gccgggggtg aggtcgctga gggcccgcgc gagatgtttt 7
ccttgctcag cacggtgcaa cccagttta cagttcctct gagtcctctc atcaatgcct 67
tccatacacc aaaaaaact tctgtttctc tcagtggagt gtcagtttct caaaaccagc 127
atcgagatgt agttcctgag catgaggctc ccagcagtga gtgtatgttc agtgacttcc 187
tgacgaagct taacattggt tcaatcggca aaggaaaaat attcgaaggg tacagatcca 247
tgttcatgga gccagcaaaa aggatgaaga agagcttgga cacaaccgat aactggcaca 307
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gacatcattc aagagctctt caaagcattt gttcagatct tcagtactgg ccagttttca 607
tacagctctg gggttttaaa actttgaaat caaggacacg acgtctccag tctacctccg 667
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tcattcttga tgtagtgtaa ttgaagggtg tgaaatgctt tgtcaatcat ttgtcacatt 2467
tatccagttt gggttattct cattatgaca cctattgcaa attagcatcc catggcaaat 2527
atattttgaa aaaataaaga actatcagga ttgaaaacag ctcttttgag gaatgtcaat 2587
(SEQ ID NO:1, Position -53 to 2587)

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## FIG. 1B

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tagttattaa gttgaaagta attaatgatt ttatgttttg ttactctact agatttgata 2647
aaaattgtgc ctttagcctt ctatatacat cagtggaaac ttaagatgca gtaattatgt 2707
tccagattga ccatgaataa aatatttttt aatctaaatg tagagaagtt gggattaaaa 2767
gcagcctcgg aaacacagag ccaggaatat agcctttttg catggtgccca tggctcacat 2827
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gaccagcctg gccaacgtgg tgaaacgctg tctctactaa aatacaaaaa aatagggctg 2947
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ctgagggtcaa gagtttgaga ccagcctggc caacatgggtg aaaccccatc tctactaaac 3067
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aggcaggaga attgcttgag cctgggagat ggagggttgca gtgagctgag atcatgccac 3187
tgactccag cctgggcaac agagcaagac tctgectcaa aaaaaaatta aaataaattt 3247
aaatacaaaa aaaaatagcc aggtgtgggg tgcatgcctg gaatcccagc tacttgagag 3307
gctgaggcac gagaattgct tgaacccagg aggtggagggt tgcagtgagc caagatcaca 3367
ggagccactg cactccagcc tgggtgacag agtgagactc tgtctcaaaa aaaaaattaa 3427
ataaattatt ataacctttc agaaatgctg tgtgcatttt catgttcttt ttttagcat 3487
tactgtcact ctccctaag aaatgtactt cagagaagca gtattttgtt aaataaatac 3547
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aaaattaaac aaaaatctca gtccctccg aagtgaactt tgtgttacc tgcgtcagaa 3667
atgccaaagt gtgtttactt ttcattcaga ttttgtgaat atgaacatgc tggtatagga 3727
tctacagatg aatattttaac tcaatagaaa aattatttta gaacacattg tattggtatt 3787
tacaaccaga ttatattctt gacgttgact tcattaaaat t 3828

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(SEQ ID NO: 1, Position 2647 to 3828)

# FIG. 1C

Met	Phe	Ser	Leu	Ser	Ser	Thr	Val	Gln	Pro	Gln	Phe	Thr	Val	Pro	Leu
1				5				10						15	
Ser	His	Leu	Ile	Asn	Ala	Phe	His	Thr	Pro	Lys	Asn	Thr	Ser	Val	Ser
			20					25					30		
Leu	Ser	Gly	Val	Ser	Val	Ser	Gln	Asn	Gln	His	Arg	Asp	Val	Val	Pro
		35					40					45			
Glu	His	Glu	Ala	Pro	Ser	Ser	Glu	Cys	Met	Phe	Ser	Asp	Phe	Leu	Thr
	50					55				60					
Lys	Leu	Asn	Ile	Val	Ser	Ile	Gly	Lys	Gly	Lys	Ile	Phe	Glu	Gly	Tyr
65				70						75				80	
Arg	Ser	Met	Phe	Met	Glu	Pro	Ala	Lys	Arg	Met	Lys	Lys	Ser	Leu	Asp
			85						90					95	
Thr	Thr	Asp	Asn	Trp	His	Ile	Arg	Pro	Glu	Pro	Phe	Ser	Leu	Ser	Ile
			100					105					110		
Pro	Pro	Ser	Leu	Asn	Leu	Arg	Asp	Leu	Gly	Leu	Ser	Glu	Leu	Lys	Ile
		115					120					125			
Gly	Gln	Ile	Asp	Gln	Leu	Val	Glu	Asn	Leu	Leu	Pro	Gly	Phe	Cys	Lys
	130					135					140				
Gly	Lys	Asn	Ile	Ser	Ser	His	Trp	His	Thr	Ser	His	Val	Ser	Ala	Gln
145				150						155					160
Ser	Phe	Phe	Glu	Asn	Lys	Tyr	Gly	Asn	Leu	Asp	Ile	Phe	Ser	Thr	Leu
			165					170						175	
Arg	Ser	Ser	Cys	Leu	Tyr	Arg	His	His	Ser	Arg	Ala	Leu	Gln	Ser	Ile
			180					185					190		
Cys	Ser	Asp	Leu	Gln	Tyr	Trp	Pro	Val	Phe	Ile	Gln	Ser	Arg	Gly	Phe
		195					200					205			
Lys	Thr	Leu	Lys	Ser	Arg	Thr	Arg	Arg	Leu	Gln	Ser	Thr	Ser	Glu	Arg
	210					215					220				
Leu	Ala	Glu	Thr	Gln	Asn	Ile	Ala	Pro	Ser	Phe	Val	Lys	Gly	Phe	Leu
225					230					235					240
Leu	Arg	Asp	Arg	Gly	Ser	Asp	Val	Glu	Ser	Leu	Asp	Lys	Leu	Met	Lys
			245					250						255	
Thr	Lys	Asn	Ile	Pro	Glu	Ala	His	Gln	Asp	Ala	Phe	Lys	Thr	Gly	Phe
			260					265					270		
Ala	Glu	Gly	Phe	Leu	Lys	Ala	Gln	Ala	Leu	Thr	Gln	Lys	Thr	Asn	Asp
		275					280					285			
Ser	Leu	Arg	Arg	Thr	Arg	Leu	Ile	Leu	Phe	Val	Leu	Leu	Leu	Phe	Gly
	290					295					300				
Ile	Tyr	Gly	Leu	Leu	Lys	Asn	Pro	Phe	Leu	Ser	Val	Arg	Phe	Arg	Thr
305					310					315					320
Thr	Thr	Gly	Leu	Asp	Ser	Ala	Val	Asp	Pro	Val	Gln	Met	Lys	Asn	Val
			325					330						335	
Thr	Phe	Glu	His	Val	Lys	Gly	Val	Glu	Glu	Ala	Lys	Gln	Glu	Leu	Gln
			340					345					350		
Glu	Val	Val	Glu	Phe	Leu	Lys	Asn	Pro	Gln	Lys	Phe	Thr	Ile	Leu	Gly
		355					360					365			

(SEQ ID NO: 2, Position 1 to 368)

# FIG. 1D

Gly	Lys	Leu	Pro	Lys	Gly	Ile	Leu	Leu	Val	Gly	Pro	Pro	Gly	Thr	Gly	
370						375				380						
Lys	Thr	Leu	Leu	Ala	Arg	Ala	Val	Ala	Gly	Glu	Ala	Asp	Val	Pro	Phe	
385					390					395					400	
Tyr	Tyr	Ala	Ser	Gly	Ser	Glu	Phe	Asp	Glu	Met	Phe	Val	Gly	Val	Gly	
				405					410					415		
Ala	Ser	Arg	Ile	Arg	Asn	Leu	Phe	Arg	Glu	Ala	Lys	Ala	Asn	Ala	Pro	
			420					425					430			
Cys	Val	Ile	Phe	Ile	Asp	Glu	Leu	Asp	Ser	Val	Gly	Gly	Lys	Arg	Ile	
	435						440					445				
Glu	Ser	Pro	Met	His	Pro	Tyr	Ser	Arg	Gln	Thr	Ile	Asn	Gln	Leu	Leu	
450						455					460					
Ala	Glu	Met	Asp	Gly	Phe	Lys	Pro	Asn	Glu	Gly	Val	Ile	Ile	Ile	Gly	
465					470					475					480	
Ala	Thr	Asn	Phe	Pro	Glu	Ala	Leu	Asp	Asn	Ala	Leu	Ile	Arg	Pro	Gly	
				485					490					495		
Arg	Phe	Asp	Met	Gln	Val	Thr	Val	Pro	Arg	Pro	Asp	Val	Lys	Gly	Arg	
			500					505					510			
Thr	Glu	Ile	Leu	Lys	Trp	Tyr	Leu	Asx	Lys	Xaa	Lys	Phe	Asp	Gln	Ser	
		515					520					525				
Val	Asp	Pro	Glu	Ile	Ile	Ala	Arg	Gly	Thr	Val	Gly	Phe	Ser	Gly	Ala	
530						535					540					
Glu	Leu	Glu	Asn	Leu	Val	Asn	Gln	Ala	Ala	Leu	Lys	Ala	Ala	Val	Asp	
545				550						555					560	
Gly	Lys	Glu	Met	Val	Thr	Met	Lys	Glu	Leu	Glu	Phe	Ser	Lys	Asp	Lys	
			565					570						575		
Ile	Leu	Met	Gly	Pro	Glu	Arg	Arg	Ser	Val	Glu	Ile	Asp	Asn	Lys	Asn	
		580					585						590			
Lys	Thr	Ile	Thr	Ala	Tyr	His	Glu	Ser	Gly	His	Ala	Ile	Ile	Ala	Tyr	
	595					600						605				
Tyr	Thr	Lys	Asp	Ala	Met	Pro	Ile	Asn	Lys	Ala	Thr	Ile	Met	Pro	Arg	
610						615					620					
Gly	Pro	Thr	Leu	Gly	His	Val	Ser	Leu	Leu	Pro	Glu	Asn	Asp	Arg	Trp	
625				630						635					640	
Asn	Glu	Thr	Arg	Ala	Gln	Leu	Leu	Ala	Gln	Met	Asp	Val	Ser	Met	Gly	
				645					650					655		
Gly	Arg	Val	Ala	Glu	Glu	Leu	Ile	Phe	Gly	Thr	Asp	His	Ile	Thr	Thr	
		660						665					670			
Gly	Ala	Ser	Ser	Asp	Phe	Asp	Asn	Ala	Thr	Lys	Ile	Ala	Lys	Arg	Met	
	675					680						685				
Val	Thr	Lys	Phe	Gly	Met	Ser	Glu	Lys	Leu	Gly	Val	Met	Thr	Tyr	Ser	
690						695					700					
Asp	Thr	Gly	Lys	Leu	Ser	Pro	Glu	Thr	Gln	Ser	Ala	Ile	Glu	Gln	Glu	
705				710							715				720	
Ile	Arg	Ile	Leu	Leu	Arg	Asp	Ser	Tyr	Glu	Arg	Ala	Lys	His	Ile	Leu	
			725						730					735		
Lys	Thr	His	Ala	Lys	Glu	His	Lys	Asn	Leu	Ala	Glu	Ala	Leu	Leu	Thr	
		740						745					750			
Tyr	Glu	Thr	Leu	Asp	Ala	Lys	Glu	Ile	Gln	Ile	Val	Leu	Glu	Gly	Lys	
	755						760					765				
Lys	Leu	Glu	Val	Arg												
770																

(SEQ ID NO: 2, Position 369 to 773)

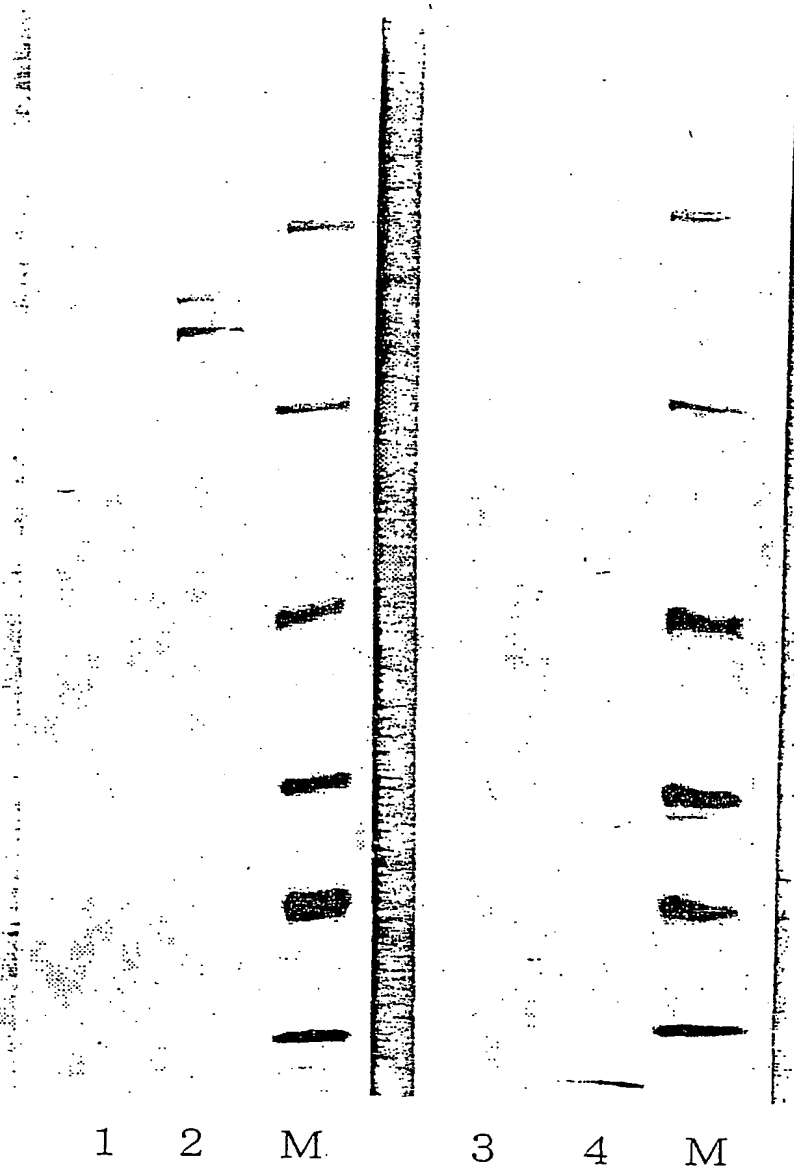
ATP binding motif

Minimum AAA protein motif

walker B binding motif

Zn binding motif

Figure 2



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Figure 3

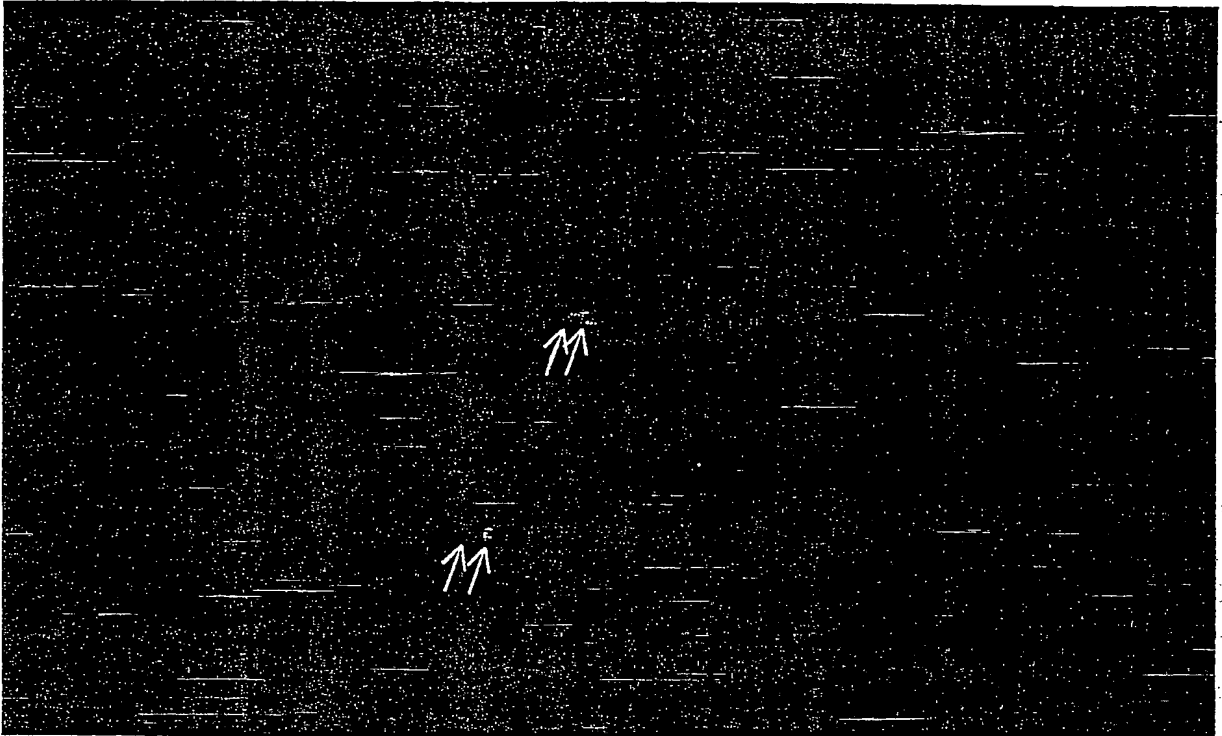
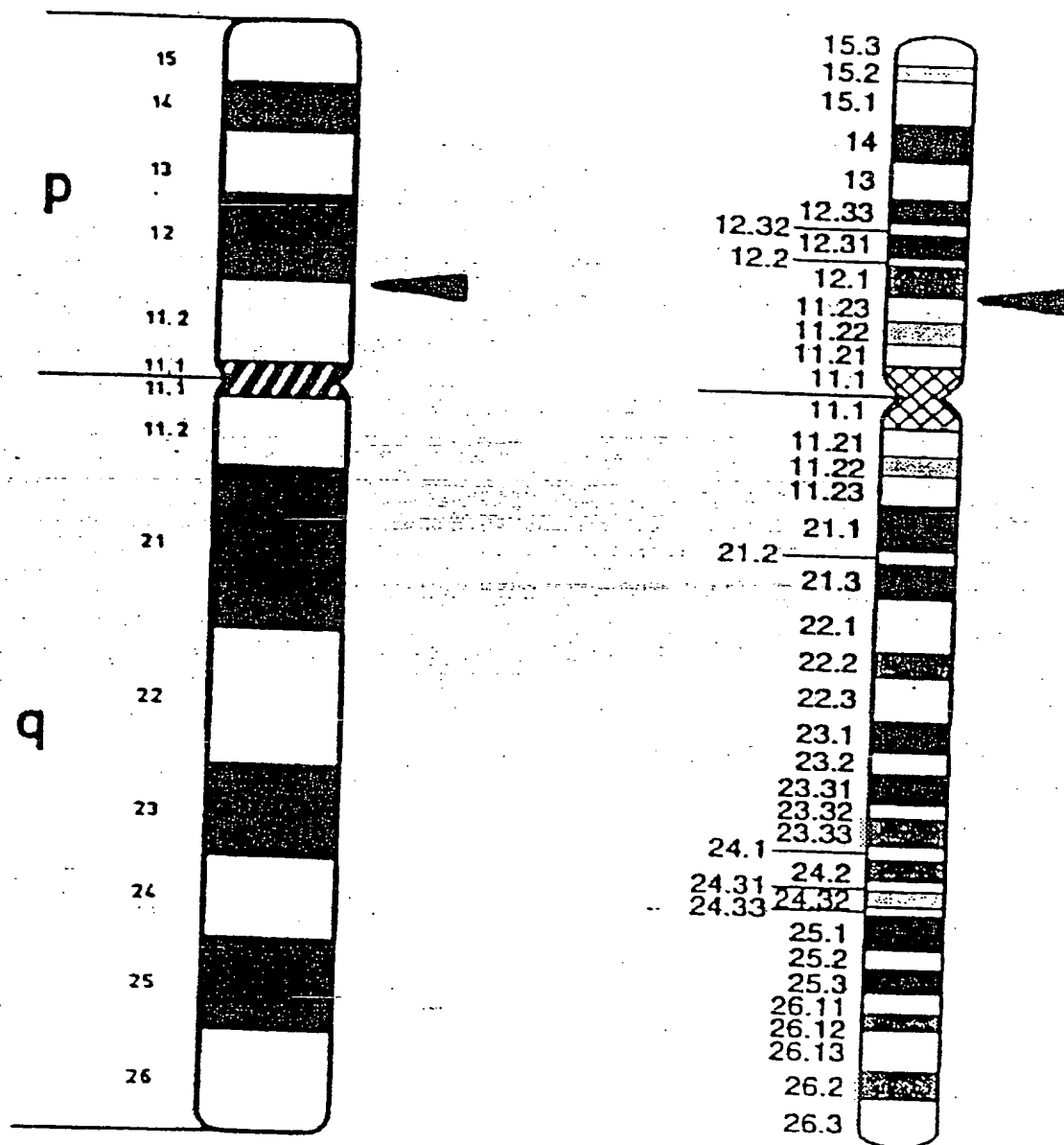


Figure 4



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